World-wide Web (ERI Chromosome 21 Sequence Database) Processing this sequence by existing exon predicting programs (programs A and B) resulted in the prediction of four sequences (exon 1: SEQ ID NO: 1; exon 2: SEQ ID NO: 2; exon 3: SEQ ID NO: 3; exon 4: SEQ ID NO: 4) as exon nucleotide sequences. The machine used to predict the exons was a SUN Ultra 60 (2 GB memory),, and the prediction time was about 5 minutes per sequence with program A (mail server) and about 10 minutes with program B (local server).

D2

IN THE CLAIMS:

Please cancel claims 5, 21, 23, 25, 26 and 27 without prejudice or disclaimer, and substitute claims 1, 2, 4, 6 - 8, 11, 19, 20, 22, 24 and 28 with the following amended claims:

1. A primer design system, comprising:

D3

SUB E1

means for selecting a plurality of different DNA nucleotide sequences from a database including a plurality of different DNA nucleotide sequences of the human genome; and

a control unit for controlling the system, said control unit controlling:

means for extracting a plurality of partial sequences meeting extraction conditions from the plurality of different DNA nucleotide sequences, wherein said extraction conditions include a predetermined base length, the database including exons dentified for the DNA nucleotide sequences stored therein;

means for determining positions of said plurality of partial sequences related to each one of said different DNA nucleotide sequences, each of said plurality of different partial sequences being extracted from different exons of the same gene;

means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said position determining means;

means for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with said different DNA nucleotide sequences from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted.

2. A primer design system according to claim 1, wherein said control unit further controls a second means for selecting a plurality of primers meeting certain selection conditions from said plurality of partial sequences extracted by said extracting means after selecting a plurality of different partial sequences.

4. A primer design system according to claim 1, wherein said control unit further controls means for limiting the plurality of different DNA nucleotide sequences, the data for which were obtained by said selecting means, to a base length longer than said predetermined base length, to be output to said extracting means.

6. A primer design system according to claim 1, further comprising a second database including data on a plurality of different DNA nucleotide sequences, said second database comprising at least one of data on cDNA nucleotide sequences included in said first database and data on the exon nucleotide sequences predicted on the basis of genomic DNA nucleotide sequences included in said first database, wherein said extracting means targets nucleotide sequences included in said second database for extraction.

7. A storage medium having recorded thereon a program executable at a control unit in a computer with memory recording data on a plurality of different DNA nucleotide sequences of the human genome, said program comprising instructions

for reading data on a plurality of different DNA nucleotide sequences in said memory,

for extracting a plurality of partial sequences meeting extraction conditions from said plurality of different DNA nucleotide sequences and the data on said plurality of different DNA nucleotide sequences, wherein said extraction conditions include a predetermined base length, the data on said plurality of different DNA nucleotide sequences including exons identified for the DNA nucleotide sequences,

for determining positions of said plurality of partial sequences related to each one of said different DNA nucleotide sequences, each of said plurality of different partial sequences being extracted from different exons of the same gene,

for selecting a plurality of different partial sequences from results of the determining step, and

for determining a plurality pairs of primers for normal PCR for each of said plurality of different partial sequences, and

for automatically collating said plurality of pairs of primers with said different DNA nucleotide sequences from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted.

8. A method for designing primers, comprising the steps of:

(a) taking data on a plurality of different DNA nucleotide sequences from a database including a plurality of different DNA nucleotide sequences of the human genome;

(b) extracting a plurality of partial sequences meeting extraction conditions from each of said plurality of different DNA nucleotide sequences based on said data, wherein said extraction conditions include a predetermined base length, said data including exons identified for the plurality of DNA nucleotide sequences;

(c) determining positions of said plurality of partial sequences related to each one of said plurality of different DNA nucleotide sequences;

(d) selecting a plurality of different partial sequences from said plurality of partial sequences, each of said plurality of different partial sequences being extracted from different exons of the same gene;

(e) after the step (d), determining a plurality pairs of primers for normal PCR for each of said plurality of different partial sequences, and

(f) automatically collating said plurality of pairs of primers with said different DNA nucleotide sequences from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted.

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11. A method for designing primers, comprising the steps of

(a) taking data on a plurality of different DNA nucleotide sequences from a database including a plurality of DNA nucleotide sequences of the human genome;

(b) extracting a plurality of partial sequences meeting extraction conditions from each of said plurality of different DNA nucleotide sequences based on said data, wherein said extraction conditions include a predetermined base length, the database including exons identified for the DNA nucleotide sequences stored therein;

(c) determining certain conditions related to positions of said plurality of partial sequences related to each one of said plurality of different DNA nucleotide sequences;

(d) selecting a plurality of different partial sequences from said plurality of partial sequences; each of said plurality of different partial sequences being extracted from different exons of the same gene;

(e) after the step (d), determining a plurality pairs of primers for normal PCR for each of said plurality of different partial sequences; and

(f) analyzing a sample DNA using as an indicator for the type of primer affording PCR amplified fragments among said plurality of primers with a storage medium,

wherein said storage medium comprises recorded data on said plurality pairs of primers, genetic data on DNA fragments amplified by PCR using said plurality pairs of primers, and said plurality of pairs of primers automatically collated with said different DNA nucleotide sequences from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted.

19. A primer design system, comprising:

D8

SUB E3

means for selecting a plurality of different DNA nucleotide sequences based on at least one predetermined genetic function of interest from a database having data on a plurality of DNA nucleotide sequences of the human genome; and

a control unit for controlling the system, said control unit controlling:

means for extracting a plurality of partial sequences meeting certain base length extraction conditions from the plurality of different DNA nucleotide sequences, the database including exons identified for the DNA nucleotide sequences stored therein;

means for determining positions of said plurality of partial sequences related to each one of said plurality of different DNA nucleotide sequences;

means for selecting a plurality of different partial sequences from said plurality of partial sequences, each of said plurality of different partial sequences being extracted from different exons of the same gene; and

means for determining a plurality pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with said different DNA nucleotide sequences from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted.

D8

20. A primer design system, comprising:

D9

means for selecting a plurality of different DNA nucleotide sequences from a database including a plurality of DNA nucleotide sequences of the human genome; and

SUB E4

a control unit for controlling the system, said control unit controlling:

means for associating exons with corresponding regions in each of the plurality of different DNA nucleotide sequences;

means for extracting a plurality of partial sequences from the exons under extraction conditions, wherein said extraction conditions include a predetermined base length, the database including exons identified for the DNA nucleotide sequences stored therein;

means for collating positions of said plurality of partial sequences related to each of the exons;

means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences, wherein more than one partial sequence is associated with a genomic sequence;

means for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with at least the positions related to said different DNA nucleotide sequences from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted.

22. A storage medium having recorded thereon a program executable at a control unit in a computer with memory recording data on a plurality of different DNA nucleotide sequences of the human genome, said program comprising instructions

D10

SUB E5

for reading data on a plurality of different DNA nucleotide sequences in said memory;

for positioning exons associated with genetic functions of interest on the plurality of different DNA nucleotide sequences;

for extracting a plurality of partial sequences from the exons under extraction conditions, wherein said extraction conditions include a predetermined base length;

for collating positions of said plurality of partial sequences related to each of the exons and the genetic functions;

for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

for automatically collating said plurality of pairs of primers with at least the positions related to said different DNA nucleotide sequences from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted.

24. A method for designing primers, comprising:

(a) selecting a plurality of different DNA nucleotide sequences from a database including a plurality of DNA nucleotide sequences of the human genome;

(b) positioning exons associated with genetic functions of interest on the plurality of different DNA nucleotide sequences;

(c) extracting a plurality of partial sequences from the exons under extraction conditions, wherein said extraction conditions include a predetermined base length;

(d) collating positions of said plurality of partial sequences related to each of the exons and the genetic functions;

(e) selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

(f) determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

(g) automatically collating said plurality of pairs of primers with at least the positions related to said different DNA nucleotide sequences from which said plurality

of different partial sequences used to determine said plurality of pairs of primers were extracted.

28. A primer design system, comprising:

means for selecting a plurality of different DNA nucleotide sequences based on at least one predetermined genetic function of interest from a database having data on a plurality of DNA nucleotide sequences of the human genome; and

a control unit for controlling the system, said control unit controlling:

means for positioning exons associated with the genetic function of interest on the plurality of different DNA nucleotide sequences;

means for extracting a plurality of partial sequences from the exons under extraction conditions, wherein said extraction conditions include a predetermined base length;

means for collating positions of said plurality of partial sequences related to each of the exons and the genetic functions;

means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

means for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with at least the positions related to said different DNA nucleotide sequences from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted.